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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/785,738A

DATE: 09/12/2001

TIME: 17:11:46

Input Set : A:\198482.1.txt

Output Set: N:\CRF3\09122001\I785738A.raw

ENTERED

3 <110> APPLICANT: Sauter, Margret M
4 Lorbiecke, Rene
6 <120> TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
7 CONDITIONS
9 <130> FILE REFERENCE: 2283/201
11 <140> CURRENT APPLICATION NUMBER: 09/785,738A
12 <141> CURRENT FILING DATE: 2001-02-16
14 <150> PRIOR APPLICATION NUMBER: 60/183,572
15 <151> PRIOR FILING DATE: 2000-02-18
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 872
23 <212> TYPE: DNA
24 <213> ORGANISM: Rice
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33 caatccac atg gag aac gaa ttc cag ga aag acg gag gtg ata gaa 110
34 Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu
35 1 5 10
37 gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
38 Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
39 15 20 25 30
41 cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
42 Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
43 35 40 45
45 gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
46 Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
47 50 55 60
49 ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
50 Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
51 65 70 75
53 gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350
54 Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser
55 80 85 90
57 ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt 398
58 Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu
59 95 100 105 110
62 gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att 446
63 Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
64 115 120 125
66 cgt ata gca ctg aag aaa gga ggc atg att gtt ctg cct gca ggg atg 494
67 Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
68 130 135 140

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70 tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga      542
71 Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
72      145      150      155
74 ctg ttt gtt ggc gat cct gtt tgg aca ccc tac aac cgt ccc cat gac      590
75 Leu Phe Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
76      160      165      170
78 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa      638
79 His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
80 175      180      185      190
82 ggt gaa aat caa gca gtt gaa ggc ttc tga gggttttgtt gggctcctgc      688
83 Gly Glu Asn Gln Ala Val Glu Gly Phe
W--> 84      195      200
86 actgcggttc tatattcaac ctgaataaga tgtgctatag caatgtaaatt ttagcacagt 748
88 ggctatgggtc gccactcacc aacttgaagt gaaagattta atgatttttg ttaattctta 808
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92 tgaa      872
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96 <211> LENGTH: 199
97 <212> TYPE: PRT
98 <213> ORGANISM: Rice
100 <400> SEQUENCE: 2
101 Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu Ala Trp
102 1      5      10      15
103 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Arg Glu
104      20      25      30
105 Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly Val Ile
106      35      40      45
107 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
108      50      55      60
109 Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys Asp Val
110 65      70      75      80
111 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser Phe Phe
112      85      90      95
113 Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
114      100      105      110
115 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Ile
116      115      120      125
117 Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
118      130      135      140
119 Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
120 145      150      155      160
121 Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
122      165      170      175
123 Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu Gly Glu
124      180      185      190
125 Asn Gln Ala Val Glu Gly Phe
126      195
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 980

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132 <212> TYPE: DNA
133 <213> ORGANISM: Rice
135 <220> FEATURE:
136 <221> NAME/KEY: CDS
137 <222> LOCATION: (139)..(735)
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142 aggctatccg gaatcgggag ggtttcccaa taggaaagca actcaggact caggagcggc 120
144 gtctgagagg ttccagag atg gag aac cag ttc cag gat ggc aag gag gag 171
145             Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu
146             1             5             10
148 gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219
149 Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
150             15             20             25
152 cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267
153 Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
154             30             35             40
156 gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat 315
157 Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
158             45             50             55
160 gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg 363
161 Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
162 60             65             70             75
164 gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag 411
165 Asp Ile Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
166             80             85             90
168 ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc 459
169 Leu Lys Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
170             95             100             105
172 tat tgt ctt gag gga agt gga tac ttc gat gtc agg gac caa aat gat 507
173 Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp
174             110             115             120
176 cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct 555
177 Gln Trp Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro
178             125             130             135
180 gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag 603
181 Ala Gly Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys
182 140             145             150             155
184 gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt 651
185 Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
186             160             165             170
188 ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc 699
189 Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile
190             175             180             185
192 aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcataatca 745
193 Asn Arg Gly Thr Gln Ala Val Glu Ala Arg
194             190             195
196 agatgtgctt cctagtccg tggttctgtta cactctacag atactgaata aactgtgcta 805
198 tcagctgttg caatgggctc ctaccgacat cttacatcat ttggcagtat tttgcacaaa 865

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200 cccgcttaaa atctccctga aaatacgcac gtcaccatgt cagagtgttt atatacaata 925
202 atgacacttc agtccacagt cagcaaggga ctaatgacaa aaaaaaaaaa aaaaa 980
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207 <212> TYPE: PRT
208 <213> ORGANISM: Rice
210 <400> SEQUENCE: 4
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212 1 5 10 15
213 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Arg Glu
214 20 25 30
215 Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser Glu Leu Gly Ile Leu
216 35 40 45
217 Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn Asp Glu Asn Leu Lys
218 50 55 60
219 Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met Asp Ile Cys Asp Val
220 65 70 75 80
221 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys Leu Lys Asn Phe Phe
222 85 90 95
223 Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
224 100 105 110
225 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Val
226 115 120 125
227 Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
228 130 135 140
229 Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
230 145 150 155 160
231 Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
232 165 170 175
233 Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile Asn Arg Gly Gly Thr
234 180 185 190
235 Gln Ala Val Glu Ala Arg
236 195
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241 <211> LENGTH: 774
242 <212> TYPE: DNA
243 <213> ORGANISM: Tomato
245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (1)..(591)
249 <400> SEQUENCE: 5
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251 Ala Pro Asp Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp
252 1 5 10 15
254 aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt 96
255 Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
256 20 25 30
258 gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt 144
259 Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu

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260          35          40          45
262 gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa 192
263 Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
264          50          55          60
266 gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa 240
267 Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
268 65          70          75          80
270 cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg 288
271 Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
272          85          90          95
274 cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt 336
275 His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
276          100          105          110
278 gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa 384
279 Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
280          115          120          125
282 ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt 432
283 Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
284          130          135          140
286 gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca 480
287 Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
288 145          150          155          160
290 att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa 528
291 Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
292          165          170          175
294 gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt 576
295 Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
296          180          185          190
298 aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt 631
299 Asn Ala Ala Ala
300          195
302 aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691
304 aatgttgat tgtggcacta aataaatcac cccctatggg agattgattg tttatatgca 751
306 agtgggaattt attatgtgat ttt 774
309 <210> SEQ ID NO: 6
310 <211> LENGTH: 196
311 <212> TYPE: PRT
312 <213> ORGANISM: Tomato
314 <400> SEQUENCE: 6
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317 Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
318          20          25          30
319 Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
320          35          40          45
321 Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
322          50          55          60
323 Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
324 65          70          75          80

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding entry.

VERIFICATION SUMMARY

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Input Set : A:\198482.1.txt

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L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:400 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:822 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17